Page 1 of 8



OIPE

RAW SEQUENCE LISTING

DATE: 07/09/2002

PATENT APPLICATION: US/10/073,300

TIME: 14:03:46

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\07092002\J073300.raw

ENTERED

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3 <110> APPLICANT: Reiter, Yoram
       5 <120> TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
       7 <130> FILE REFERENCE: 02/23339
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/073,300
 C--> 9 <141> CURRENT FILING DATE: 2002-06-25
       9 <160> NUMBER OF SEQ ID NOS: 20
      11 <170> SOFTWARE: PatentIn version 3.0
      14 <210> SEQ ID NO: 1
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    84 tcaaatttcc tgaattgcta tgtgtctggg tttcatccat ccgacattga agttgactta
                                                                              60
    86 ctgaagaatg gagagagaat tgaaaaagtg gagcattcag acttgtcttt cagcaaggac
                                                                             120
    88 tggtctttct atctcttgta ttatactgag ttcaccccca ctgaaaaaga tgagtatgcc
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240

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Input Set : A:\SEQUENCE LISTING.txt Output Set: N:\CRF3\07092002\J073300.raw

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     92 ggtggcggtg gaagcggcgg tggaggctct ggtggaggtg gcagcggctc tcactccatg
                                                                               360
     94 aggtattet teacateegt gteeeggeee ggeegegggg ageeeegett categeagtg
                                                                               420
     96 ggctacgtgg acgacacgca gttcgtgcgg ttcgacagcg acgccgcgag ccagaggatg
                                                                               480
     98 gagccgcggg cgccgtggat agagcaggag ggtccggagt attgggacgg ggagacacgg
                                                                               540
     100 aaagtgaagg cccactcaca gactcaccga gtggacctgg ggaccctgcg cggctactac
                                                                                600
     102 aaccagagcg aggccggttc tcacaccgtc cagaggatgt atggctgcga cgtggggtcg
                                                                                660
     104 gactggcgct tecteegegg gtaccaccag tacgectacg acggcaagga ttacategee
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     110 gagtggctcc gcagatacct ggagaacggg aaggagacgc tgcagcgcac ggacgcccc
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     112 aaaacgcaca tgactcacca cgctgtctct gaccatgaag ccaccctgag gtgctgggcc
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     114 ctgagettet accetgegga gateacactg acctggeage ggaettggag gaatetttga
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    141 Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu
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    144 Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr
    147 Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala
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    150 Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp
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                        85
    153 Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
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                                         105
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                115
                                    120
    159 Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp
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                                                     140
    162 Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met
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    165 Glu Pro Arg Ala Pro Trp Ile Glu Glu Glu Gly Pro Glu Tyr Trp Asp
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   174 Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe
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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\07092002\J073300.raw

177 178	Leu 225	Arg	Gly	Tyr	His	Gln 230	Туг	Ala	туг	Asp			Asp	Tyr	Ile	Ala
			G1 ₁	λαη	Tou				mb.	. 31.	235					240
181	пси	шуз	OIC	. ASP	245	hry	ser	111	, 1111			Asp	мет	. Ата		Gln
		Thr	T.vc	uic			. c1	. או	. 21-	250			a 1	-1	255	' _
184	. 1111	1111	шуз	260	ьγэ	ırp	GIU	ALd			vai	Ата	GLu			Arg
		Tur	Т.д.			The	Crra	1751	265		.		_	270	_	
187	, Alu	T Y T	275	GIU	СТУ	1111	Cys	Agr	. GLU	Trp	Leu	Arg			Leu	Glu
		C1**			mb.~		a 1	280				_	285			
190	non	290	пуs	GIU	1111	Leu	295	Arg	Thr	Asp	А А Та		Lys	Thr	His	Met
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193	305	1113	птэ	нта	val	310	ASP	HIS	GIU	Ата		Leu	Arg	Cys	Trp	Ala
			Dho	Пттъ	Dwo			T 1 -	ml		315	_				320
196	пси	Der	FIIC	TÄT	325	нта	GIU	116	Thr			Trp	GIn	Arg		Gly
		λen	Cln	Пhх			m b	a 1	T	330		1		_	335	
199	Giu	ASP	GIII	340	GIII	Asp	THE	GIU			GIu	Thr	Arg		Ala	Gly
		C117	Thr		Cln	T ***	TT	37-	345				_	350		
202	кэр	ату	355	PHE	GTII	гуѕ	тгр	Ala	Ата	val	Val	Val		Ser	GLY	Gln
		Cln			mb~	7	77.5 -	360					365			
205	Giu	370	Alg	тут	1111	Cys	115	val	GIN	HIS	Glu		Leu	Pro	Lys	Pro
			Lou	λκα	T ren	C1	375		m l	3	a1	380		_		
207	385	1111	ьeu	AIG	ттр	390	GIN	ser	Thr	Arg	Gly	GLY	Ala	Ser	Gly	
		Τ.Δ11	C117	Clv	Tla		01. .	21.	16-4	T	395	a 3	_	_	_	400
211	GIY	ьец	СТУ	GIY	405	Pne	GIU	Ата	мет		Met	GLu	Leu	Arg		
	<210)> <1	en ti	ח או						410					415	
	<21															
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	<400					յ Տալ	JIEII.	-								
						Δra	таг	Dho	Dho	Пhт	Ser	17 n 1	a	3	D	a 1
226	1		1110	UCL	1100	Arg	1 J T	FIIE	rne	1111	26.	Val	ser	Ara		(÷137
					5									5		011
228					5					10					15	
228 229				Pro	5				Val	10	Tyr			Asp	15	
229	Arg	Gly	Glu	Pro 20	5 Arg	Phe	Ile	Ala	Val 25	10 Gly	Tyr	Val	Asp	Asp 30	15 Thr	Gln
229 231	Arg	Gly	Glu Arg	Pro 20	5 Arg	Phe	Ile	Ala Ala	Val 25	10 Gly		Val	Asp Met	Asp 30	15 Thr	Gln
229 231 232	Arg Phe	Gly Val	Glu Arg 35	Pro 20 Phe	5 Arg Asp	Phe Ser	Ile Asp	Ala Ala 40	Val 25 Ala	10 Gly Ser	Tyr Gln	Val Arg	Asp Met 45	Asp 30 Glu	15 Thr Pro	Gln Arg
229 231 232 234	Arg Phe	Gly Val Pro	Glu Arg 35	Pro 20 Phe	5 Arg Asp	Phe Ser	Ile Asp Glu	Ala Ala 40	Val 25 Ala	10 Gly Ser	Tyr	Val Arg Trp	Asp Met 45	Asp 30 Glu	15 Thr Pro	Gln Arg
229 231 232 234 235	Arg Phe Ala	Gly Val Pro 50	Glu Arg 35 Trp	Pro 20 Phe Ile	5 Arg Asp Glu	Phe Ser Gln	Ile Asp Glu 55	Ala Ala 40 Gly	Val 25 Ala Pro	10 Gly Ser Glu	Tyr Gln Tyr	Val Arg Trp 60	Asp Met 45 Asp	Asp 30 Glu Gly	15 Thr Pro Glu	Gln Arg Thr
229 231 232 234 235 237	Arg Phe Ala Arg	Gly Val Pro 50	Glu Arg 35 Trp	Pro 20 Phe Ile	5 Arg Asp Glu	Phe Ser Gln His	Ile Asp Glu 55	Ala Ala 40 Gly	Val 25 Ala Pro	10 Gly Ser Glu	Tyr Gln Tyr Arg	Val Arg Trp 60	Asp Met 45 Asp	Asp 30 Glu Gly	15 Thr Pro Glu	Gln Arg Thr
229 231 232 234 235 237 238	Arg Phe Ala Arg 65	Gly Val Pro 50 Lys	Glu Arg 35 Trp Val	Pro 20 Phe Ile Lys	5 Arg Asp Glu Ala	Phe Ser Gln His 70	Ile Asp Glu 55 Ser	Ala Ala 40 Gly Gln	Val 25 Ala Pro	10 Gly Ser Glu His	Tyr Gln Tyr Arg	Val Arg Trp 60 Val	Asp Met 45 Asp	Asp 30 Glu Gly Leu	15 Thr Pro Glu Gly	Gln Arg Thr Thr
229 231 232 234 235 237 238 240	Arg Phe Ala Arg 65	Gly Val Pro 50 Lys	Glu Arg 35 Trp Val	Pro 20 Phe Ile Lys	5 Arg Asp Glu Ala Tyr	Phe Ser Gln His 70	Ile Asp Glu 55 Ser	Ala Ala 40 Gly Gln	Val 25 Ala Pro	10 Gly Ser Glu His	Tyr Gln Tyr Arg	Val Arg Trp 60 Val	Asp Met 45 Asp	Asp 30 Glu Gly Leu	15 Thr Pro Glu Gly Val	Gln Arg Thr Thr
229 231 232 234 235 237 238 240 241	Arg Phe Ala Arg 65 Leu	Gly Val Pro 50 Lys Arg	Glu Arg 35 Trp Val Gly	Pro 20 Phe Ile Lys Tyr	5 Arg Asp Glu Ala Tyr 85	Phe Ser Gln His 70 Asn	Ile Asp Glu 55 Ser Gln	Ala Ala 40 Gly Gln Ser	Val 25 Ala Pro Thr	10 Gly Ser Glu His Ala 90	Tyr Gln Tyr Arg 75 Gly	Val Arg Trp 60 Val Ser	Asp Met 45 Asp Asp	Asp 30 Glu Gly Leu Thr	15 Thr Pro Glu Gly Val 95	Gln Arg Thr Thr 80 Gln
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229 231 232 234 235 237 238 240 241 243 244 246 247	Arg Phe Ala Arg 65 Leu Arg	Gly Val Pro 50 Lys Arg Met	Glu Arg 35 Trp Val Gly Tyr Gln 115	Pro 20 Phe Ile Lys Tyr Gly 100 Tyr	Arg Asp Glu Ala Tyr 85 Cys Ala	Phe Ser Gln His 70 Asn Asp	Ile Asp Glu 55 Ser Gln Val Asp	Ala Ala 40 Gly Gln Ser Gly Gly 120	Val 25 Ala Pro Thr Glu Ser 105 Lys	10 Gly Ser Glu His Ala 90 Asp	Tyr Gln Tyr Arg 75 Gly Trp	Val Arg Trp 60 Val Ser Arg	Asp Met 45 Asp Asp His Phe Ala 125	Asp 30 Glu Gly Leu Thr Leu 110 Leu	15 Thr Pro Glu Gly Val 95 Arg	Gln Arg Thr Thr 80 Gln Gly Glu
229 231 232 234 235 237 238 240 241 243 244 246 247	Arg Phe Ala Arg 65 Leu Arg Tyr Asp	Gly Val Pro 50 Lys Arg Met	Glu Arg 35 Trp Val Gly Tyr Gln 115	Pro 20 Phe Ile Lys Tyr Gly 100 Tyr	Arg Asp Glu Ala Tyr 85 Cys Ala	Phe Ser Gln His 70 Asn Asp Tyr	Ile Asp Glu 55 Ser Gln Val Asp Ala	Ala Ala 40 Gly Gln Ser Gly Gly 120	Val 25 Ala Pro Thr Glu Ser 105 Lys	10 Gly Ser Glu His Ala 90 Asp	Tyr Gln Tyr Arg 75 Gly Trp Tyr Ala	Val Arg Trp 60 Val Ser Arg Ile	Asp Met 45 Asp Asp His Phe Ala 125	Asp 30 Glu Gly Leu Thr Leu 110 Leu	15 Thr Pro Glu Gly Val 95 Arg	Gln Arg Thr Thr 80 Gln Gly Glu
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255 Glu Gly Thr Cys Val Glu Trp Leu Arg Tyr Leu Glu Asn Gly Lys 256 170 258 Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His 180 185 261 Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe 200 264 Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln 215 220 267 Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr 268 225 230 235 270 Phe Gln Lys Trp Ala Ala Val Val Pro Ser Gly Gln Glu Gln Arg 245 250 273 Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu 260 265 276 Arg Trp Glu Gln Ser Thr Arg Gly 277 275 279 <210> SEQ ID NO: 7 281 <211> LENGTH: 100 283 <212> TYPE: PRT 285 <213> ORGANISM: Homo sapiens 289 <400> SEQUENCE: 7 291 Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala 294 Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His 20 297 Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu 40 300 Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr 55 303 Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala 70 306 Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp 309 Asp Arg Asp Met 310 312 <210> SEQ ID NO: 8 314 <211> LENGTH: 36 316 <212> TYPE: DNA C--> 318 <213> ORGANISM: Artificial 322 <220> FEATURE: 324 <223> OTHER INFORMATION: synthetic oligonucleotide 326 <400> SEQUENCE: 8 327 aggagatata catatgggct ctcactccat gaggta 36 330 <210> SEQ ID NO: 9 332 <211> LENGTH: 43 334 <212> TYPE: DNA C--> 336 <213> ORGANISM: Artificial 340 <220> FEATURE: 342 <223> OTHER INFORMATION: synthetic oligonucleotide

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